dis his full

(FILE 'HOME' ENTERED AT 09:35:01 ON 25 APR 2007)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT
09:36:18 ON 25 APR 2007
L1   99 SEA ABB=ON   PLU=ON   ALICYCLOBACILLUS AND PCR
L2   16 SEA ABB=ON   PLU=ON   L1 AND REAL-TIME
L3   7 DUP REM L2 (9 DUPLICATES REMOVED)
              DIS 33 1-7 IBIB
              DIS L3 2-7 IBIB
L4   13 SEA ABB=ON   PLU=ON   L1 AND TAQMAN
              DIS L4 ALL IBIB
              DIS L4 2-14 IBIB
L5   51 SEA ABB=ON   PLU=ON   L1 AND 16S
L6   22 DUP REM L5 (29 DUPLICATES REMOVED)
              DIS L6 1-22 IBIB

FILE 'STNGUIDE' ENTERED AT 09:48:01 ON 25 APR 2007

FILE HOME

FILE MEDLINE
 FILE LAST UPDATED: 24 Apr 2007 (20070424/UP).   FILE COVERS 1950 TO DATE.

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   substance identification.

FILE BIOSIS
FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 18 April 2007 (20070418/ED)

FILE CAPLUS

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FILE COVERS 1907 - 25 Apr 2007   VOL 146 ISS 18
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 FILE COVERS 1974 TO 24 Apr 2007 (20070424/ED)

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   and biweekly.

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FILE SCISEARCH

FILE COVERS 1974 TO 19 Apr 2007 (20070419/ED)

SCISEARCH has been reloaded, see HELP RLOAD for details.

FILE AGRICOLA

FILE COVERS 1970 TO 3 Apr 2007 (20070403/ED)

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FILE STNGUIDE
FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Apr 20, 2007 (20070420/UP).

=>

Sequence Alignments.

1. Sequence alignment of Hristova's primers and probes to the PM1 16S ribosomal RNA gene alignment

```
963F    1     CCTTGACATGTCTAGAAGTTACCAGAGA  28
              ||||||||||||||||||||||||||||
16S     963   CCTTGACATGTCTAGAAGTTACCAGAGA  990


1076R   1     GCGGGACTTAACCCAACATCT  21
              |||||||||||||||||||||
16s     1076  GCGGGACTTAACCCAACATCT  1056


1030T   1     ACACGAGCTGACGACGGCCATG  22
              ||||||||||||||||||||||
16S     1011  ACACGAGCTGACGACGGCCATG  990
```

2. Sequence alignments of 10/727261 SEQ ID NOs: 1, 2 and 4:

RESULT 9 (SEQ ID NO: 1) FORWARD PRIMER
ID   ADW05721
```
Qy        1 GAGCCCGCGGCGCATTAGC 19
            |||||||||||||||||||
Db      214 GAGCCCGCGGCGCATTAGC 232
```

RESULT 27 (SEQ ID NO: 4) REVERSE PRIMER
ADW05721/c
```
Qy        1 GCTTGCGCCCATTGCG 16
            ||||||||||||||||
Db      369 GCTTGCGCCCATTGCG 354
```

RESULT 76 (SEQ ID NO: 2) PROBE
ADW05721
```
Qy        1 GCGACGATGCGTAGCCG 17
            |||||||||||||||||
Db      260 GCGACGATGCGTAGCCG 276
```

3. SEQ ID NO:78 (10/727/261) and Alicyclobacillus and Geobacillus rDNA alignments, and SEQ ID NOs: 1,2 and 4 alignments. See pages (2-9).

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.16 [Mar-25-2007]
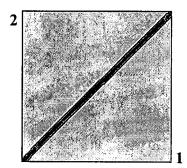
Match: [1] Mismatch: [-2] gap open: [5] gap extension: [2]
x_dropoff: [0] expect: [10.0000] wordsize: [11] Filter ☑ View option [Standard ▼]
Masking character option [X for protein, n for nucleotide ▼] Masking color option [Black ▼]
☐ Show CDS translation [Align]

Sequence 1: lcl|seq_1
Length = 1498 (1 .. 1498)   SEQ ID # 48

Sequence 2: gi|18496336|dbj|AB042058.1|Alicyclobacillus acidoterrestris gene for 16S ribosomal RNA, partial sequence.
Length = 1514 (1 .. 1514)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.


```
 Score = 2619 bits (1362),  Expect = 0.0
 Identities = 1450/1498 (96%), Gaps = 3/1498 (0%)
 Strand=Plus/Plus

Query  1    AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGC  60
            |.||||||||||||||||||||||||||||||.|||||||||||||||||||||||||||
Sbjct  1    AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGC  60

Query  61   GGGCCCTTCGGGGCCAGCGGCGGACGGGTGAGTAACACGTGGGTAATCTGCCTTTCAGAC  120
            .|.|||||||||||.|||||||||||||||||||||||||||||||.||||||||||||||
Sbjct  61   GAGCCCTTCGGGGCTAGCGGCGGACGGGTGAGTAACACGTGGGCAATCTGCCTTTCAGAC  120

Query  121  CGGAATAACGCCCGGAAACGGGTGCTAATGCCGGATANGCACGCGAGNAGGCATCTNCTT  180
```

```
            |||||||||| | |||||||||||||||||||||||||||||    || || | ||||||||| |||
Sbjct  121  TGGAATAACACTCGGAAACGGGTGCTAATGCCGGATAAT-ACACGGGTAGGCATCTACTT  179

Query  181  GCGGGGAAAGGTGCAANTGCATCGCTGAGAGAGGAGCCCGCGGCGCATTAGCTAGTTGGT  240
            | |   ||||| |||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  180  GTGTTGAAAGATGCAACTGCATCGCTGAGAGAGGAGCCCGCGGCGCATTAGCTAGTTGGT  239

Query  241  GGGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACAC  300
            | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240  GAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACAC  299

Query  301  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300  TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATG  359

Query  361  GGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGAAGAAGGCCTTCGGGTTGTAAAGCTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  360  GGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGAAGAAGGCCTTCGGGTTGTAAAGCTC  419

Query  421  TGTTGCTCGGGGAGAGCGGCAAGGGGAGTGGAAAGCCCCTTGNGAGACGGTACCGAGTGA  480
            |||||||||||||||||||| |||||| |||||||||| ||||| |||||||||||||||
Sbjct  420  TGTTGCTCGGGGAGAGCGACAAGGAGAGTGGAAAGCTCCTTGTGAGACGGTACCGAGTGA  479

Query  481  GGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  480  GGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTC  539

Query  541  CGGAATCACTGGGCGTAAAGCGTGCGTAGGCGGTTGNGTAAGTCTGGAGTGAAAGTCCAN  600
            ||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||||
Sbjct  540  CGGAATCACTGGGCGTAAAGCGTGCGTAGGCGGTTGTGTAAGTCTGAAGTGAAAGTCCAA  599

Query  601  GGCTCAACCNTGGGAATGCTTTGGAAACTGCNTGACTTGAGTGCTGGAGAGGCAAGGGGA  660
            ||||||||| ||||| ||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  600  GGCTCAACCTTGGGATTGCTTTGGAAACTGCATGACTTGAGTGCTGGAGAGGCAAGGGGA  659

Query  661  ATTCCNCGTGTAGCGGTGNAATGCGTAGATATGTGGAGGAATACCAGTGGCGAANGCGCC  720
            ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||| |||||
Sbjct  660  ATTCCACGTGTAGCGGTGAAATGCGTAGATATGTGGAGGAATACCAGTGGCGAAGGCGCC  719

Query  721  TTGCTGGACAGTGACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATAC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720  TTGCTGGACAGTGACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATAC  779

Query  781  CCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGGGGACACACCCCAGTGCC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  780  CCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGGGGACACACCCCAGTGCC  839

Query  841  GAAGGAAACCCAATAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  840  GAAGGAAACCCAATAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGG  899

Query  901  AATTGACGGGGGCCCGCACAAGCAGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGA  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  900  AATTGACGGGGGCCCGCACAAGCAGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGA  959

Query  961  ACCTTACCAGGGCTNGACATCCCTCTGACAGCCGCAGAGATGNGGNTTCCCTTCGGGGCA  1020
            |||||||||||||| ||||||||||||||| | ||||||| |     ||||||||||||||
Sbjct  960  ACCTTACCAGGGCTTGACATCCCTCTGACCGGTGCAGAGATGTACCTTCCCTTCGGGGCA  1019

Query  1021 GAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1080
```

SEQ ID # 1 Forward primer.

SEQ ID # 2 probe

SEQ ID # 4 Reverse primer